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Fig. 1a

GAATTCGCGG CCGCCTCTTG CGGTCCCAGA GTGGAGTGA AGGTCTGGAG CTTTGGGAGG	60
AGACGGGGAG GACAGACTGG AGGCGTGTTT CTCCCGGATT TTCTTTTTCG TGCGAGCCCT	120
CGCGCGCGCG TACAGTCATC CCGCTGGTCT GACGATTGTG GAGAGCGGT GGAGAGGCTT	180
CATCCATCCC ACCCGGTCGT CGCCGGGGAT TGGGGTCCA GCGACACCTC CCCGGGAGAA	240
GCAGTGCCCA GGAAGTTTTC TGAAGCCGGG GAAGCTGTGC AGCCGAAGCC GCCGCCGCGC	300
CGGAGCCCGG GACACCGGCC ACCCTCCGCG CCACCCACCC TCGCTTCTC CGGCTTCCTC	360
TGGCCCAGGC GCCGCGCGGA CCCGGCAGCT GTCTGCCAC GCCGAGCTCC ACGGTGAAAA	420
AAAAAGTGAA GGTGTAAGAG CAGCACAAGT GCAATAAGAG ATATTTCCTC AAATTGCGCT	480
CAAG ATG GAA ACC CTT TGC CTC AGG GCA TCC TTT TGG CTG GCA CTG GTT	529
Met Glu Thr Leu Cys Leu Arg Ala Ser Phe Trp Leu Ala Leu Val	
-20 -15 -10	577
GGA TGT GTA ATC AGT GAT AAT CCT GAG AGA TAC AGC ACA AAT CTA AGC	
Gly Cys Val Ile Ser Asp Asn Pro Glu Arg Tyr Ser Thr Asn Leu Ser	
-5 -1 1 5 10	
AAT CAT GTG GAT GAT TTC ACC ACT TTT CGT GGC ACA GAG CTC AGC TTC	625
Asn His Val Asp Asp Phe Thr Thr Phe Arg Gly Thr Glu Leu Ser Phe	
15 20 25	
CTG GTT ACC ACT CAT CAA CCC ACT AAT TTG GTC CTA CCC AGC AAT GGC	673
Leu Val Thr Thr His Gln Pro Thr Asn Leu Val Leu Pro Ser Asn Gly	
30 35 40	
TCA ATG CAC AAC TAT TGC CCA CAG CAG ACT AAA ATT ACT TCA GCT TTC	721
Ser Met His Asn Tyr Cys Pro Gln Gln Thr Lys Ile Thr Ser Ala Phe	
45 50 55	
AAA TAC ATT AAC ACT GTG ATA TCT TGT ACT ATT TTC ATC GTG GGA ATG	769
Lys Tyr Ile Asn Thr Val Ile Ser Cys Thr Ile Phe Ile Val Gly Met	
60 65 70 75	

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Fig. 1b

GTG GGG AAT GCA ACT CTG CTC AGG ATC ATT TAC CAG AAC AAA TGT ATG	817
Val Gly Asn Ala Thr Leu Leu Arg Ile Ile Tyr Gln Asn Lys Cys Met	
80 85 90	
AGG AAT GGC CCC AAC GCG CTG ATA GCC AGT CTT GCC CTT GGA GAC CTT	865
Arg Asn Gly Pro Asn Ala Leu Ile Ala Ser Leu Ala Leu Gly Asp Leu	
95 100 105	
ATC TAT GTG GTC ATT GAT CTC CCT ATC AAT GTA TTT AAG CTG CTG GCT	913
Ile Tyr Val Val Ile Asp Leu Pro Ile Asn Val Phe Lys Leu Leu Ala	
110 115 120	
GGG CGC TGG CCT TTT GAT CAC AAT GAC TTT GGC GTA TTT CTT TGC AAG	961
Cly Arg Trp Pro Phe Asp His Asn Asp Phe Gly Val Phe Leu Cys Lys	
125 130 135	
CTG TTC CCC TTT TTG CAG AAG TCC TCG GTG GGG ATC ACC GTC CTC AAC	1009
Leu Phe Pro Phe Leu Gln Lys Ser Ser Val Gly Ile Thr Val Leu Asn	
140 145 150 155	
CTC TGC GCT CTT AGT GTT GAC AGG TAC AGA GCA GTT GCC TCC TGG AGT	1057
Leu Cys Ala Leu Ser Val Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser	
160 165 170	
CGT GTT CAG GGA ATT GGG ATT CCT TTG GTA ACT GCC ATT GAA ATT GTC	1105
Arg Val Gln Gly Ile Gly Ile Pro Leu Val Thr Ala Ile Glu Ile Val	
175 180 185	
TCC ATC TGG ATC CTG TCC TTT ATC CTG GCC ATT CCT GAA GCG ATT GGC	1153
Ser Ile Trp Ile Leu Ser Phe Ile Leu Ala Ile Pro Glu Ala Ile Gly	
190 195 200	
TTC GTC ATG GTA CCC TTT GAA TAT AGG GGT GAA CAG CAT AAA ACC TGT	1201
Phe Val Met Val Pro Phe Glu Tyr Arg Gly Glu Gln His Lys Thr Cys	
205 210 215	

Fig. 1c

ATG CTC AAT GCC ACA TCA AAA TTC ATG GAG TTC TAC CAA GAT GTA AAG 1249
Met Leu Asn Ala Thr Ser Lys Phe Met Glu Phe Tyr Gln Asp Val Lys
220 225 230 235
GAC TGG TGG CTC TTC GGG TTC TAT TTC TGT ATG CCC TTG GTG TGC ACT 1297
Asp Trp Trp Leu Phe Gly Phe Tyr Phe Cys Met Pro Leu Val Cys Thr
240 245 250
GCG ATC TTC TAC ACC CTC ATG ACT TGT GAG ATG TTG AAC AGA AGG AAT 1345
Ala Ile Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Asn Arg Arg Asn
225 260 265
GGC AGC TTG AGA ATT GCC CTC AGT GAA CAT CTT AAG CAG CGT CGA GAA 1393
Gly Ser Leu Arg Ile Ala Leu Ser Glu His Leu Lys Gln Arg Arg Glu
270 275 280
GTG GCA AAA ACA GTT TTC TGC TTG GTT GTA ATT TTT GCT CTT TGC TGG 1441
Val Ala Lys Thr Val Phe Cys Leu Val Val Ile Phe Ala Leu Cys Trp
285 290 295
TTC CCT CTT CAC TTA AGC CGT ATA TTG AAG AAA ACT GTG TAT AAC GAA 1489
Phe Pro Leu His Leu Ser Arg Ile Leu Lys Lys Thr Val Tyr Asp Glu
300 305 310 315
ATG GAC AAG AAC CGA TGT GAA TTA CTT AGT TTC TTA CTG CTC ATG GAT 1537
Met Asp Lys Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Leu Met Asp
320 325 330
TAC ATC GGT ATT AAC TTG GCA ACC ATG AAT TCA TGT ATA AAC CCC ATA 1585
Tyr Ile Gyr Ile Asn Leu Ala Thr Met Asn Ser Cys Lie Asn Pro Ile
335 340 345
GCT CTG TAT TTT GTG AGC AAG AAA TTT AAA AAT TGT TTC CAG TCA TGC 1633
Ala Leu Tyr Phe Val Ser Lys Lys Phe Lys Asn Cys Phe Gln Ser Cys
350 355 360

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Fig. 1d

CTC TGC TGC TGC TGT TAC CAG TCC AAA AGT CTG ATG ACC TCG GTC CCC 1681
Leu Cys Cys Cys Cys Tyr Gln Ser Lys Ser Leu Met Thr Ser Val Pro
365 370 375
ATG AAC GGA ACA AGC ATC CAG TGG AAG AAC CAC GAT CAA AAC AAC CAC 1729
Met Asn Gly Thr Ser Ile Gln Trp Lys Asn His Asp Gln Asn Asn His
380 385 390 395
AAC ACA GAC CGG AGC AGC CAT AAG GAC AGC ATG AAC TGACCACCCT 1775
Asn Thr Asp Arg Ser Ser His Lys Asp Ser Met Asn
400 405
TAGAAGCACT CCTCGGTACT CCCATAATCC TCTCGGAGAA AAAAATCACA AGGCAACTGT 1835
GACTCCGGGA ATCTCTTCTC TGATCCTTCT TCCTTAATTC ACTCCACAC CCAAGAAGAA 1895
ATGCTTTCCA AAACCGCAAG GTAGACTGGT TTATCCACCC ACAACATCTA CGAATCGTAC 1955
TTCTTTAATT GATCTAATTT ACATATTCTG CGTGTGTAT TCAGCACTAA AAAATGGTGG 2015
GAGCTGGGGG AGAATGAAGA CTGTAAATG AAACCAGAAG GATATTTACT ACTTTTGCAT 2075
GAAAATAGAG CTTTCAAGTA CATGGCTAGC TTTTATGGCA GTTCTGGTGA ATGTTCAATG 2135
GGAAGTGGTC ACCATGAAAC TTTAGAGATT AACGACAAGA TTTTCTACTT TTTTAAAGTG 2195
ATTTTTTGTC CTTAGCCAA ACACAATATG GGCTCAGGTC ACTTTTATTT GAAATGTCAT 2255
TTGGTGCCAG TATTTTTTAA CTGCATAATA GCCTAACATG ATTATTTGAA CTTATTTACA 2315
CATAGTTTGA AAAAAAAG AAAAAATAG TATTCAGGTG AGCAATTAGA TTAGTATTTT 2375
CCACGTCCT ATTTATTTT TAAAAACACA AATTCTAAAG CTACAACAAA TACTACAGGC 2435
CCTTAAAGCA CAGTCTGATG ACACATTTGG CAGTTTAATA GATGTTACTC AAAGAATTTT 2495
TTAAGAACTG TATTTTATTT TTAAATGGT GTTTTATTAC AAGGGACCTT GAACATGTTT 2555
TGTATGTAA ATTCAAAAGT AATGCTTCAA TCAGATAGTT CTTTTTCACA AGTTCAATAC 2615
TGTTTTTCAT GTAAATTTG TATGAAAAAT CAATGTCAAG TACCAAAATG TTAATGTATG 2675
TGTCATTTAA CTCTGCCTGA GACTTTCAGT GCACTGTATA TAGAAGTCTA AAACACACCT 2735
AAGAGAAAAA GATCGAATTT TTCAGATGAT TCGGAAATTT TCATTCAGGT ATTTGTAATA 2795

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Fig. 1e

GTGACATATA TATGTATATA CATATCACCT CCTATTCTCT TAATTTTGT TAAAATGTTA 2855
ACTGGCAGTA AGTCTTTTTT GATCATTCCC TTTTCCATAT AGGAAACATA ATTTTGAAGT 2915
GGCCAGATGA GTTTATCATG TCAGTGAAAA ATAATTACCC ACAAATGCCA CCAGTAACTT 2975
AACGATTCTT CACTTCTTGG GGTTTTCAGT ATGAACCTAA CTCCCCACCC CAACATCTCC 3035
CTCCCACATT GTCACCATT TCAAAGGGCCC ACAGTGA CTGCTGGGCA TTTTCCAGA 3095
TGTTTACAGA CTGTGAGTAC AGCAGAAAAAT CTTTACTAC TGTGTGTGTG TATATATATA 3155
AACAATTGTA AATTTCTTTT AGCCCATTTT TCTAGACTGT CTCTGTGGAA TATATTTGTG 3215
TGTGTGATAT ATGCATGTGT GTGATGGTAT GTATGGATT AATCTAATCT AATAATTGTG 3275
CCCCGCAGTT GTGCCAAAGT GCATAGTCTG AGCTAAAATC TAGGTGATTG TTCATCATGA 3335
CACCCTGCCT CAGTCCATT TAACCTGTAG CAACCTCTG CATTACATAA TCTTGTAATC 3395
ATGTTACCAT TACAAATGGG ATATAAGAGG CAGCGTGAAA GCAGATGAGC TGTGGACTAG 3455
CAATATAGGG TTTTGTTTGG TTGGTTGGTT TGATAAAGCA GTATTTGGGG TCATATTGTT 3515
TCCTGTGCTG GAGCAAAAGT CATTACACTT TGAAGTATTA TATTGTTCTT ATCCTCAATT 3575
CAATGTGGTG ATGAAATTGC CAGGTGTCT GATATTTCTT TCAGACTTCG CCAGACAGAT 3635
TGCTGATAAT AAATTAGGTA AGATAATTG TTGGGCCATA TTTTAGGACA GGTAAAATAA 3695
CATCAGGTTT CAGTTGCTTG AATTGCAAGG CTAAGAAGTA CTGCCCTTTT GTGTGTTAGC 3755
AGTCAAATCT ATTATTCCAC TGGCGCATCA TATGCAGTGA TATATGCCTA TAATATAAGC 3815
CATAGGTTCA CACCATTTTG TTTAGACAAT TGTCTTTTTT TCAAGATGCT TTGTTTCTTT 3875
CATATGAAAA AAATGCATTT TATAAATTCA GAAAGTCATA GATTTCTGAA GCGTCAACG 3935
TGCAATTTAT TTATGGACTG GTAAGTAACT GTGGTTTACT AGCAGGAATA TTTCCAATTT 3995
CTACCTTTAC TACATCTTTT CAACAAGTAA CTTTGTAGAA ATGAGCCAGA AGCCAAGGCC 4055
CTGAGTTGGC AGTGGCCCAT AAGTGTA AAAAGTTTA CAGAAACCTT 4105

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Fig. 2a

GAGACATTCC GGTGGGGGAC TCTGGCCAGC CCGAGCAACG TGGATCCTGA GAGCACTCCC	60
AGGTAGGCAT TTGCCCCGGT GGGACGCCTT GCCAGACCAG TGTGTGGCAG GCCCCCGTGG	120
AGGATCAACA CAGTGGCTGA ACACTGGGAA GGAAGTGGTA CTTGGAGTCT GGACATCTGA	180
AACTTGGCTC TGAAACTGCG GAGCGGCCAC CGGACGCCTT CTGGAGCAGG TAGCAGC	237
ATG CAG CCG CCT CCA AGT CTG TGC GGA CGC GCC CTG GTT GCG CTG GTT	285
Met Gln Pro Pro Pro Ser Leu Cys Gly Arg Ala Leu Val Ala Leu Val	
1 5 10 15	
CTT GCC TGC GGC CTG TCG CGG ATC TGG GGA GAG GAG AGA GGC TTC CCG	333
Leu Ala Cys Gly Leu Ser Arg Ile Trp Gly Glu Glu Arg Gly Phe Pro	
20 25 30	
CCT GAC AGG GCC ACT CCG CTT TTG CAA ACC GCA GAG ATA ATG ACG CCA	381
Pro Asp Arg Ala Thr Pro Leu Leu Gln Thr Ala Glu Ile Met Thr Pro	
35 40 45	
CCC ACT AAG ACC TTA TGG CCC AAG GGT TCC AAC GCC AGT CTG GCG CGG	429
Pro Thr Lys Thr Leu Trp Pro Lys Gly Ser Asn Ala Ser Leu Ala Arg	
50 55 60	
TCG TTG GCA CCT GCG GAG GTG CCT AAA GGA GAC AGG ACG GCA GGA TCT	477
Ser Leu Ala Pro Ala Glu Val Pro Lys Gly Asp Arg Thr Ala Gly Ser	
65 70 75 80	
CCG CCA CGC ACC ATC TCC CCT CCC CCG TGC CAA GGA CCC ATC GAG ATC	525
Pro Pro Arg Thr Ile Ser Pro Pro Pro Cys Gln Gly Pro Ile Glu Ile	
85 90 95	
AAG GAG ACT TTC AAA TAC ATC AAC ACG CTT GTG TCC TGC CTT GTG TTC	573
Lys Glu Thr Phe Lys Tyr Ile Asn Thr Val Val Ser Cys Leu Val Phe	
100 105 110	

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Fig. 2b

GTG CTG GGG ATC ATC GGG AAC TCC ACA CTT CTG AGA ATT ATC TAC AAG	621
Val Leu Gly Ile Ile Gly Asn Ser Thr Leu Leu Arg Ile Ile Tyr Lrs	
115 120 125	
AAC AAG TGC ATG CGA AAC GGT CCC AAT ATC TTG ATC GCC AGC TTG GCT	669
Asn Lys Gys Met Arg Asn Gly Pro Asn Ile Leu Ile Ala Ser Leu Ala	
130 135 140	
CTG GGA GAC CTG CTG CAC ATC GTC ATT GAC ATC CCT ATC AAT GTC TAC	717
Leu Gly Asp Leu Leu His Ile Val Ile Asp Ile Pro Ile Asn Val Tyr	
145 150 155 160	
AAG CTG CTG GCA GAG GAC TGG CCA TTT GGA GCT GAG ATG TGT AAG CTG	765
Lys Leu Leu Ala Glu Asp Trp Pro Phe Gly Ala Glu Met Cys Lys Leu	
165 170 175	
GTG CCT TTC ATA CAG AAA GCC TCC GTG GGA ATC ACT GTG CTG AGT CTA	813
Val Pro Phe Ile Gln Lys Ala Ser Val Gly Ile Thr Val Leu Ser Leu	
180 185 190	
TGT GCT CTG AGT ATT GAC AGA TAT CGA GCT GTT GCT TCT TGG AGT AGA	861
Cys Ala Leu Ser Ile Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser Arg	
195 200 205	
ATT AAA GGA ATT GGG GTT CCA AAA TGG ACA GCA GTA GAA ATT GTT TTG	909
Ile Lys Gly Ile Gly Val Pro Lys Trp Thr Ala Val Glu Ile Val Leu	
210 215 220	
ATT TGG GTG GTC TCT GTG GTT CTG GCT GTC CCT GAA GCC ATA GGT TTT	957
Ile Trp Val Val Ser Val Val Leu Ala Val Pro Glu Ala Ile Gly Phe	
225 230 235 240	
GAT ATA ATT ACG ATG GAC TAC AAA GGA AGT TAT CTG CGA ATC TGC TTG	1005
Asp Ile Ile Thr Met Asp Tyr Lys Gly Ser Tyr Leu Arg Ile Cys Leu	
245 250 255	

Fig. 2c

CTT CAT CCC GTT CAG AAG ACA GCT TTC ATG CAG TTT TAC AAG ACA GCA	1053
Leu His Pro Val Gln Lys Thr Ala Phe Met Gln Phe Tyr Lys Thr <u>Ala</u>	
260 265 270	
AAA GAT TGG TGG CTG TTC AGT TTC TAT <u>TTC</u> TGC TTG CCA TTG GCC ATC	1101
Lys Asp Tyr Trp Leu Phe Ser Phe Tyr Phe Cys Leu Pro Leu Ala Ile	
275 280 285	
ACT GCA TTT TTT TAT ACA CTA ATG ACC TGT GAA ATG TTG AGA AAG AAA	1149
Thr Ala Phe Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Arg Lys Lys	
290 295 300	
AGT GGC ATG CAG ATT GCT TTA AAT GAT CAC CTA AAG CAG AGA CGG GAA	1197
Ser Gly Met Gln Ile Ala Leu Asn Asp His Leu Lys Gln Arg Arg Glu	
305 310 315 320	
GTG GCC AAA ACC GTC TTT TGC CTG GTC CTT GTC TTT GCC CTC TGC TGG	1245
Val Ala Lys Thr Val Phe Cys Leu Val Leu Val Phe Ala Leu Cys Trp	
325 330 335	
CTT CCC CTT CAC <u>CTC</u> AGC AGG ATT CTG AAG CTC ACT GTT TAT AAT CAG	1293
Leu Pro Leu His Leu Ser Arg Ile Leu Lys Leu Thr Leu Tyr Asp Gln	
340 345 350	
AAT GAT CCC AAT AGA TGT GAA CTT TTG AGC TTT CTG TTG GTA TTG GAC	1341
Asn Asp Pro Asn Arg Cys Glu Leu Leu Ser Phe Leu Leu Val Leu Asp	
355 360 365	
TAT ATT GGT ATG AAC <u>ATG</u> GCT TCA CTG AAT TCC TGC ATT AAC CCA ATT	1389
Tyr Ile Gyr Ile Asn Met Ala Ser Leu Asn Ser Cys Ile Asn Pro Ile	
370 375 380	
GCT CTG TAT TTC GTG AGC AAA AGA TTC AAA AAC TGC TTT AAG TCA TGC	1437
Ala Leu Tyr Leu Val Ser Lys Arg Phe Lys Asn Cys Phe Lys Ser Cys	
385 390 395 400	

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Fig. 2d

TTA TGC TGC TGG TGC CAG TCA TTT GAA GAA AAA CAG TCC TTG GAG GAA 1485
Leu Cys Cys Trp Cys Gln Ser Phe Glu Glu Lys Gln Ser Leu Glu Glu
405 410 415
AAG CAG TCG TGC TTA AAG TTC AAA GCT AAT GAT CAC GGA TAT GAC AAC 1533
Lys Gln Ser Cys Leu Lys Phe Lys Ala Asn Asp His Gly Tyr Asp Asn
420 425 430
TTC CGT TCC AGT AAT AAA TAC AGC TCA TCT TGAAAGAAGA ACTATTCAC 1583
Phe Arg Ser Ser Asn Lys Tyr Ser Ser Ser
435 440
GTATTTTCATT TTCTTTATAT TGGACGGAAG TCATTA[•]AAAC AAAATGAAAC ATTTGCCAAA 1643
ACAAAACAAA AAACATGTG TTTGCACAGC ACACTATTAA[•] AATATTAAGT GTAATTATTT 1703
TAACACTCAC AGCTACATAT GACATTTTAT GAGCTGTTTA CGGCATGGAA AGAAAATCAG 1763
AGGGAATTAA GAAAGCCTCG TCGTGAAAGC ACTTAATTTT TTACAGTTAG CACTTCAACA 1823
TAGCTCTTAA CAACTTCCAG GATATTCACA CAACACTTAG GCTTAAAAAT GAGCTCACTC 1883
AGAATTTCTA TTCTTTCTAA AAAGAGATTI[•] ATTTTAAAT CAATGGGACT CTGATATAAA 1943
GGAAGAATAA GTCACTGTAA AACAGAACTT TTAAATGAAG CTAAATTAC TCAATTIAAA 2003
ATTTTAAAT CCTTTAAAC AACTTTTCAA TTAATATTAT CACACTATTA TCAGATTGTA 2063
ATTAGATGCA AATGAGAGAG CAGTTTAGTT GTTGCAATTT TCGGACACTG GAAAGATTI[•]A 2123
AATGATCAGG AGGGAGTAAC AGAAAGAGCA AGGCTGTTTT TGAAATTCAT TACACTTTCA 2183
CTAGAAGCCC AAACCTCAGC ATTCTGCAAT ATGTAACCAA CATGTCACAA ACAAGCAGCA 2243
TGTAACAGAC TGGCACATGT GCCAGCTGAA[•] TTTAAAATAT AATACTTTTA AAAAGAAAAT 2303
TATTACATCC TTTACATTCA GTTAAGATCA AACCTCACAA AGAGAAATAG AATGTTTGAA 2363
AGGCTATCCC AAAAGACTTT TTTGAATCTG TCATTCACAT ACCCTGTGAA GACAATACTA 2423
TCTACAATTT TTTCAGGATT ATTA[•]AAATCT TCTTTTTTCA CTATCGTAGC TTAAACTCTG 2483
TTTGTTTTTG TCATCTGTAA AACTTACCT ACATACACTG CATGTAGATG ATTAATGAG 2543
GGCAGGCCCT GTGCTCATAG CTTTACGATG GAGAGATGCC AGTGACCTCA TAATAAGAC 2603
TGTGA[•]ACTGC CTGGTGCA[•]GT GTCCACATGA CAAAGGGGCA GGTAGCACCC TCTCTACCC 2663

Fig. 2e

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ATGCTGTGGT TAAATGGTT TCTAGCATAT GTATAATGCT ATAGTAAAA TACTATTTTT 2723
CAAAATCATA CAGATTAGTA CATTTAACAG CTACCTGTAA AGCTTATTAC TAATTTTTGT 2783
ATTATTTTTG TAAATAGCCA ATAGAAAAGT TTGCTTGACA TGGTGCTTTT CTTTCATCTA 2843
GAGGCAAAAC TGCTTTTTGA GACCGTAAGA ACCTCTTAGC TTTGTGCGTT CCTGCCTAAT 2903
TTTTATATCT TCTAAGCAAA GTGCCTTAGG ATAGCTTGGG ATGAGATGTG TGTGAAAGTA 2963
TGTACAAGAG AAAACGGAAG AGAGAGGAAA TGAGGTGGGG TTGGAGGAAA CCCATGGGGA 3023
CAGATTCCCA TTCTTAGCCT AACGTTGTC ATTGCCTCGT CACATCAATG CAAAAGGTCC 3083
TGATTTTGTT CCAGCAAAAC ACAGTGCAAT GTTCTCAGAG TGA~~CTTT~~CGA AATAATTGG 3143
GCCAAGAGC TTTAACTCGG TCTTAAATA TGCCCAAATT TTTACTTTGT TTTTCTTTTA 3203
ATAGGCTGGG CCACATGTTG GAAATAAGCT AGTAATGTTG TTTTCTGTCA ATATTGAATG 3263
TGATGGTACA GTAAACCAAA ACCCAACAAT GTGGCCAGAA AGAAAGAGCA ATAATAATTA 3323
ATTCACACAC CATATGGATT CTATTTATAA ATCACCACAA AACTTGTCT TTAATTTTAT 3383
CCCAATCACT TTTTCAGAGG CCTGTTATCA TAGAAGTCAT TTAGACTCT CAATTTTAAA 3443
TTAATTTTGA ATCACTAATA TTTTCACAGT TTATTAATAT ATTTAATTC TATTTAATT 3503
TTAGATTATT TTTATTACCA TGACTGAAT TTTTACATCC TGATACCTT TCCTTCTCCA 3563
TGTCAGTATC ATGTTCTCTA ATTATCTTGC CAAATTTTGA AACTACACAC AAAAAGCATA 3623
CTTGCA~~TTAT~~ TTATAATAAA ATTGCATTCA GTGGCTTTTT AAAAAAATG TTTGATTCAA 3683
AACTTTAACA TACTGATAAG TAAGAAACAA TTATAATTC TTTACATACT CAAAACCAAG 3743
ATAGAAAAAG GTGCTATCGT TCAACTTCAA AACATGTTTC CTAGTATTAA GGACTTTAAT 3803
ATAGCAACAG ACAAATTAT TGTTAACATG GATGTTACAG CTCAAAGAT TTATAAAGA 3863
TTTTAACCTA TTTTCTCCCT TATTATCCAC TGCTAATGTG GATGTATGTT CAAACACCTT 3923
TTAGTATTGA TAGCTTACAT ATGGCCAAAG GAATACAGTT TATAGCAAAA CATGGGTATG 3983
CTGTAGCTAA CTTTATAAAA GTGTAATATA ACAATGTAAA AAATTATATA TCTGGGAGGA 4043
TTTTTTGGTT GCCTAAAGTG GCTATAGTTA CTGATTTTTT ATTATGTAAG CAAAACCA~~AT~~ 4103
AAAAATTTAA GTTTTTTTAA CAACTACCTT ATTTTCACT GTACAGACAC TAATTCATTA 4163
AATACTAATT GATTGTTTAA AAGAAATATA AATGTGACAA GTGGACATTA TTTATGTTAA 4223
ATATACAATT ATCAAGCAAG TATGAAGTTA TTCA~~ATTAAA~~ ATGCCACATT TCTGGTCTCT 4283
GGGAAAAAAA AAAAAAAA 4301

0994571660

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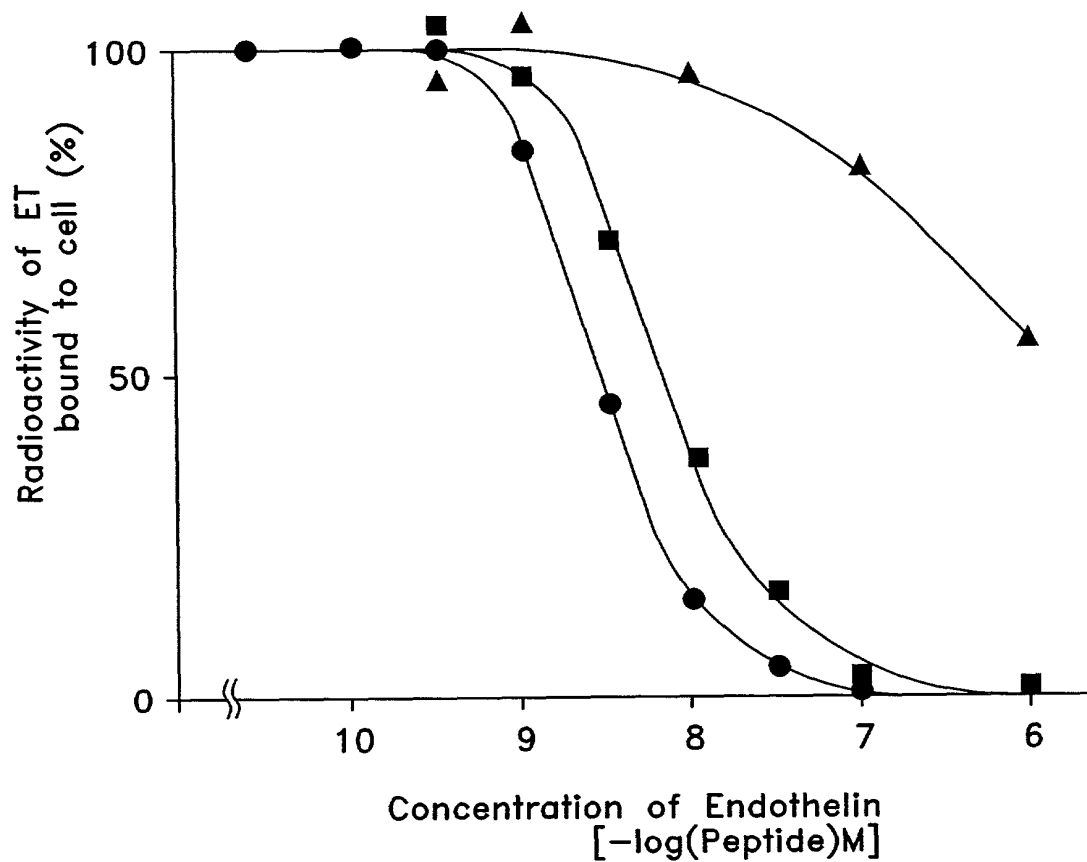


Fig. 3

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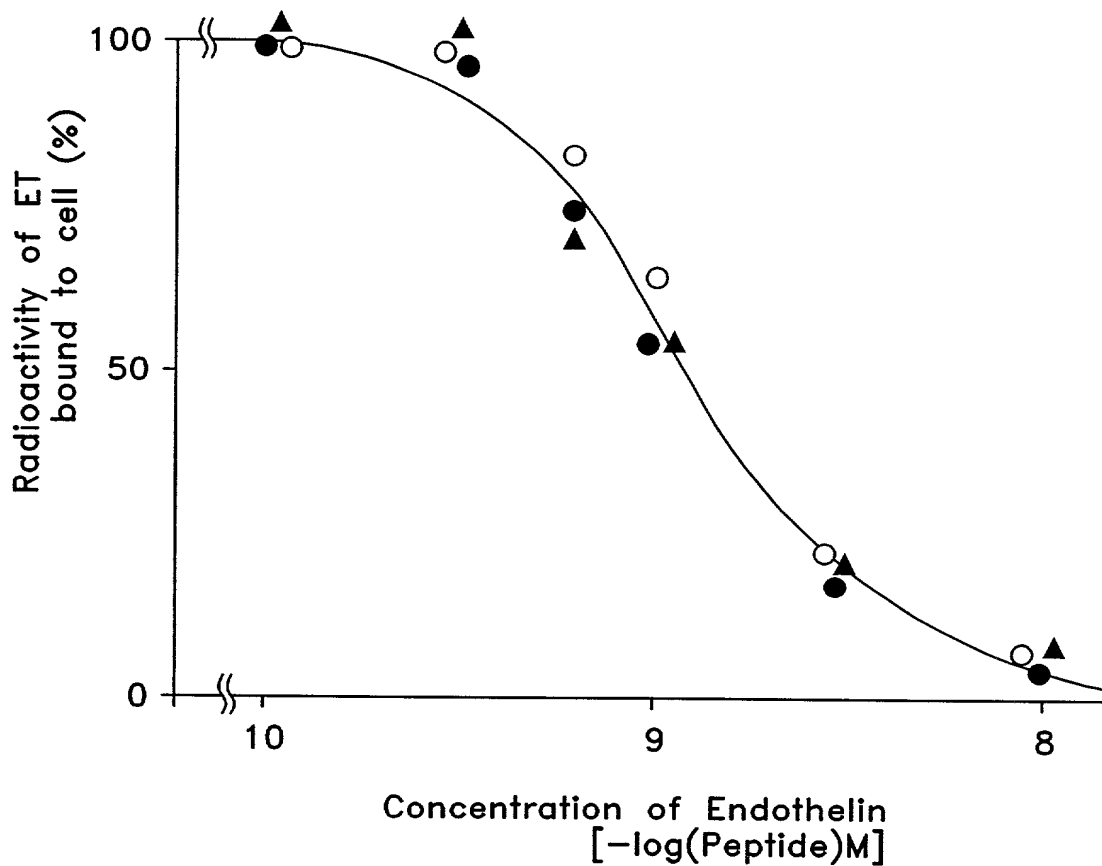


Fig. 4

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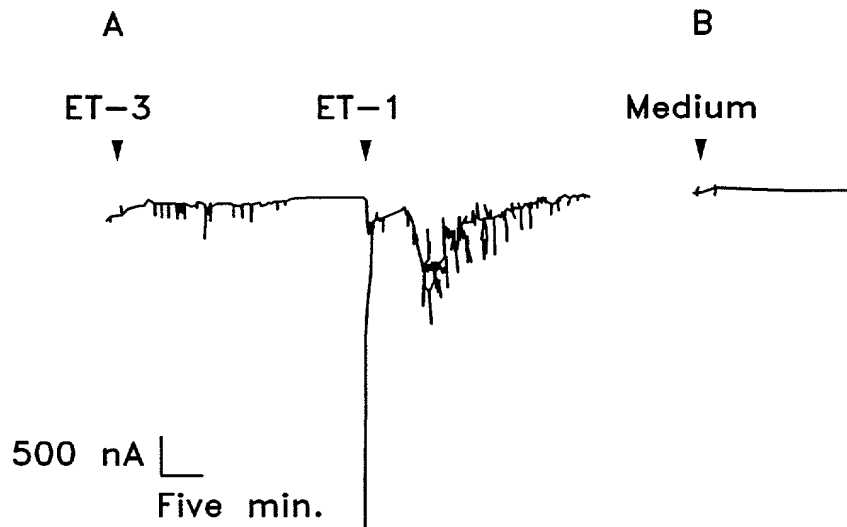
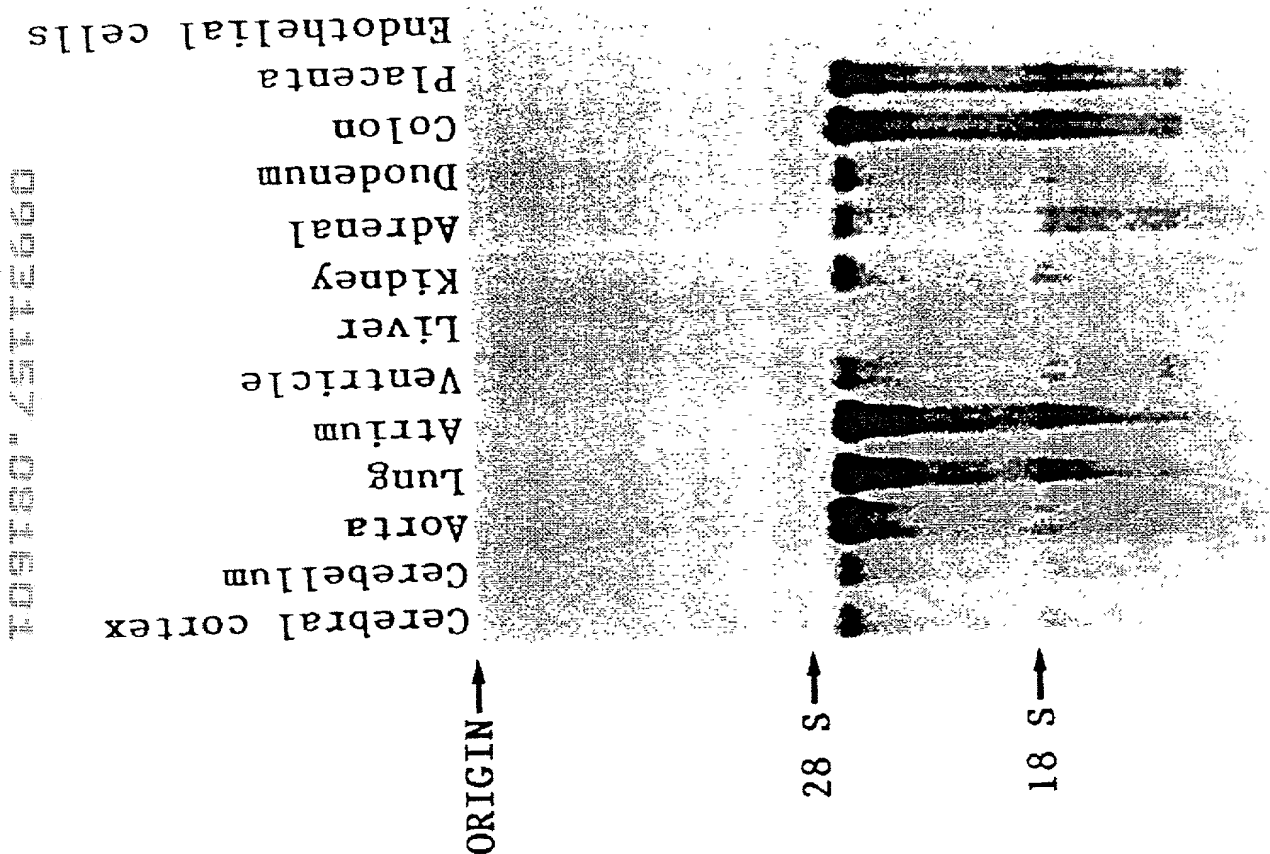


Fig. 5

Fig. 6



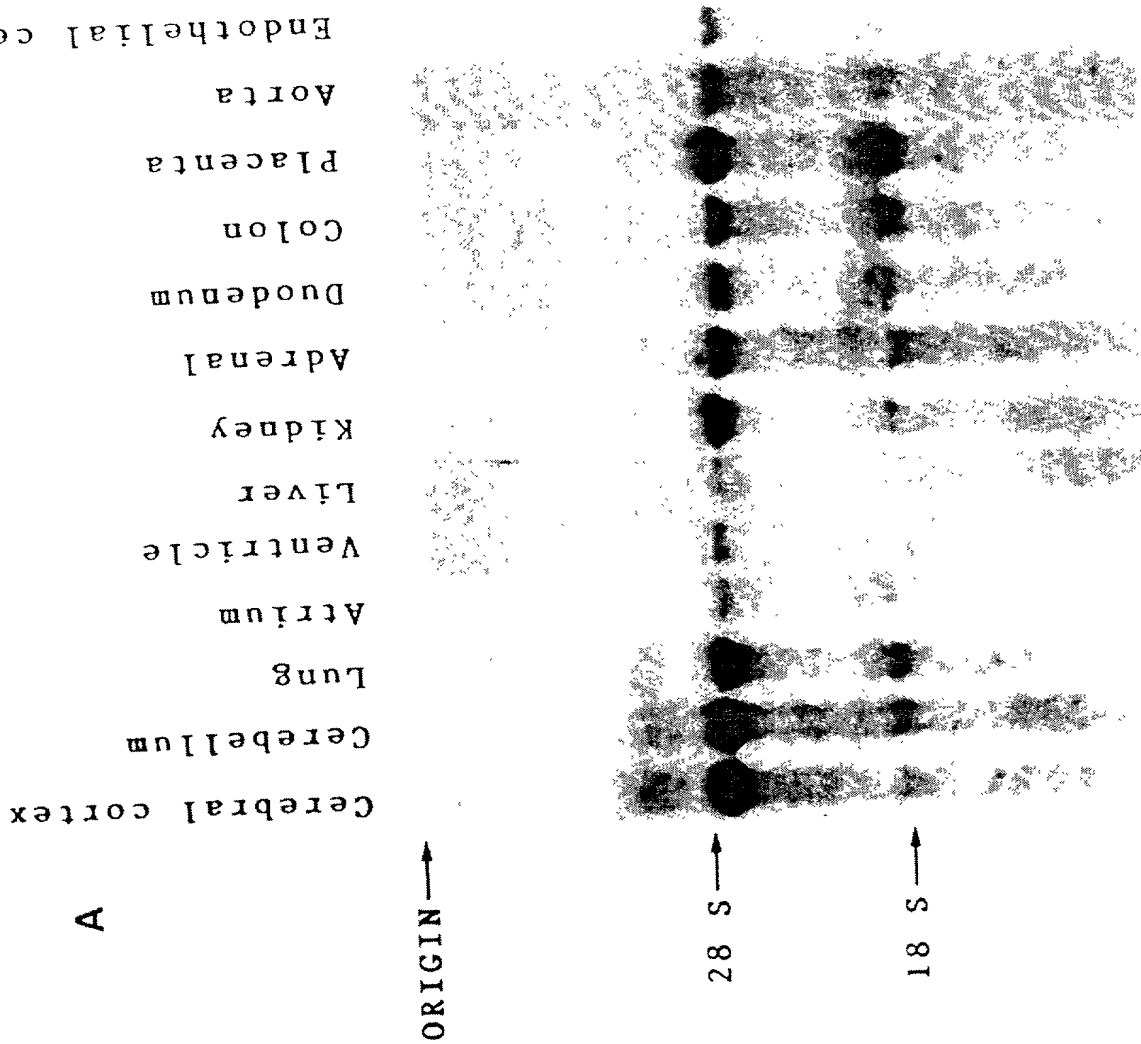


Fig. 7

[illegible]

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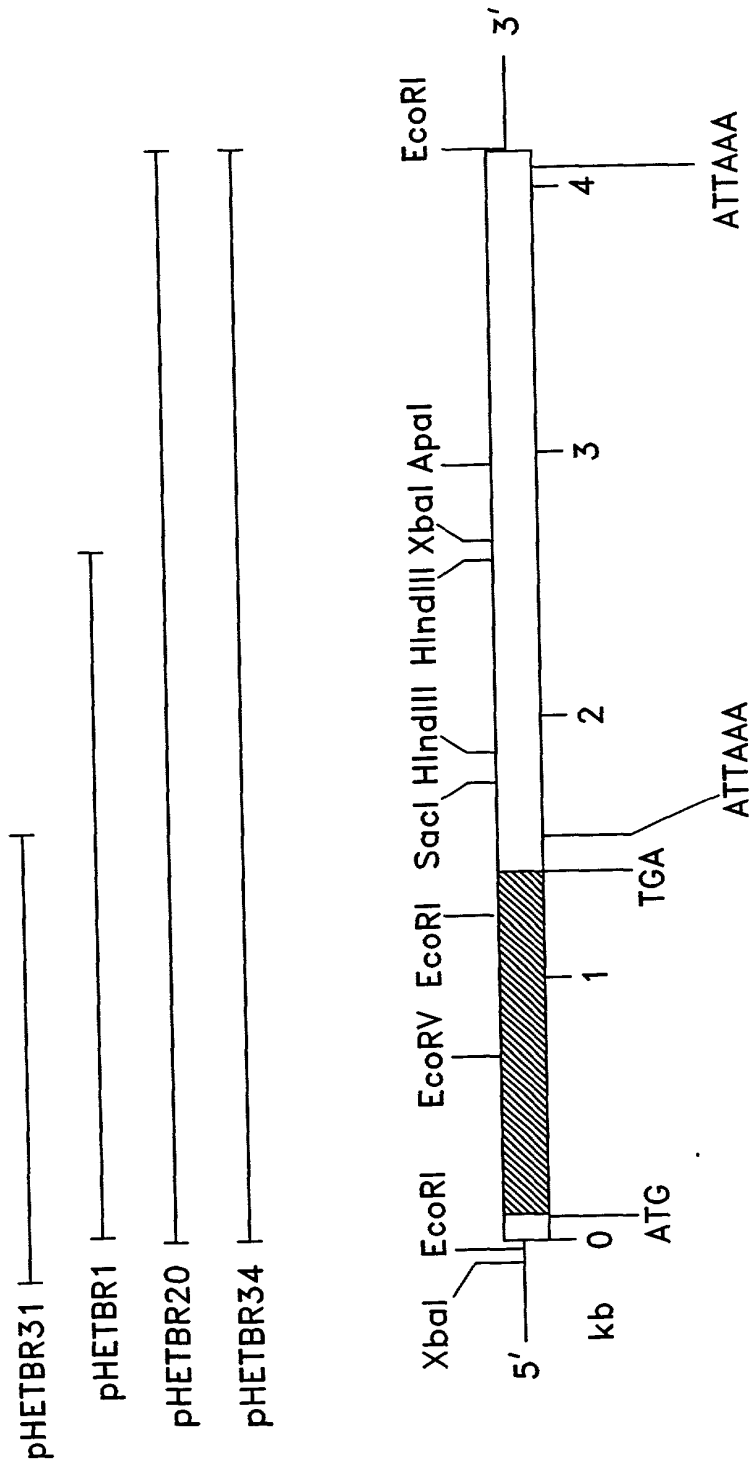


Fig. 8